

FIG. 1A

40

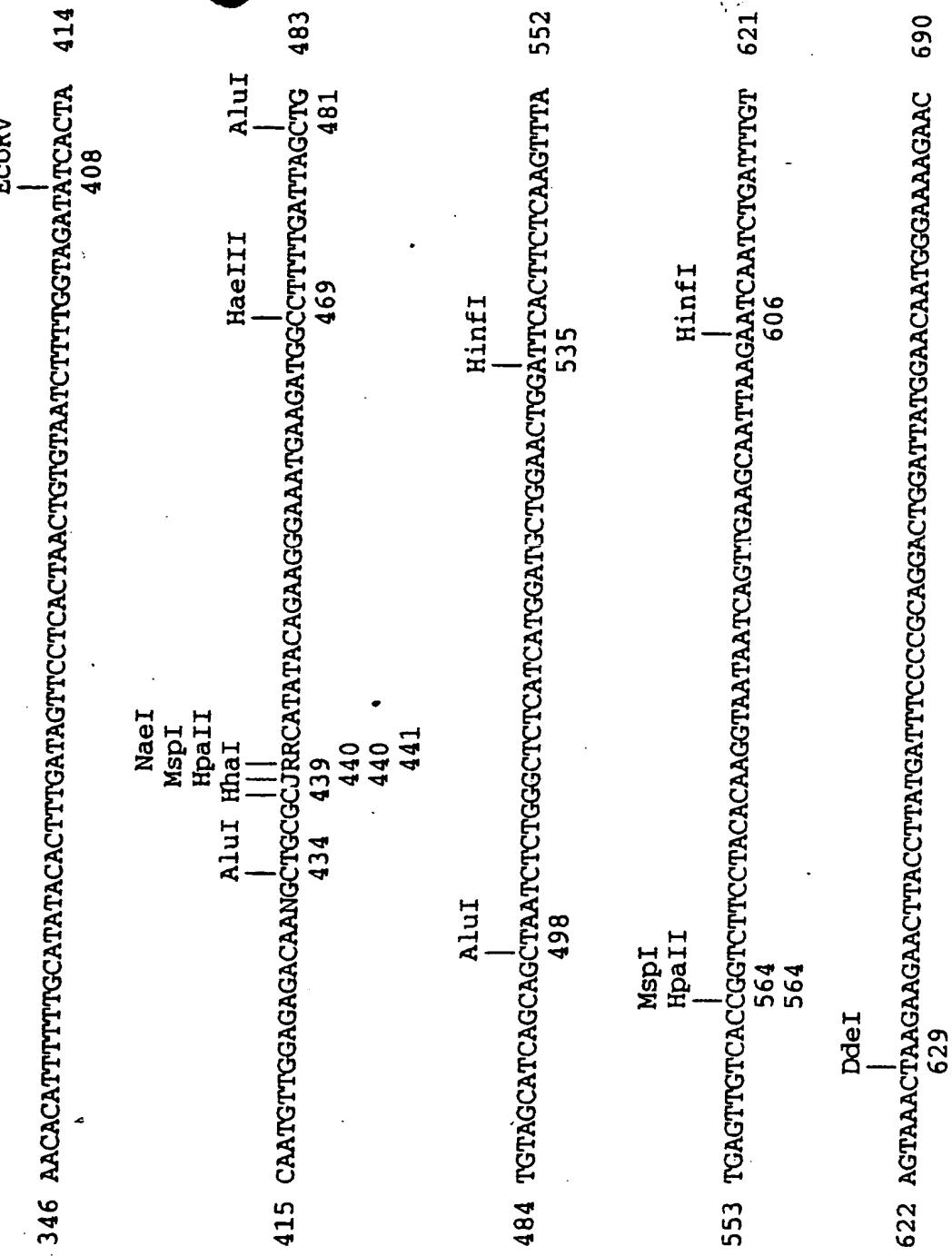


FIG. 1B

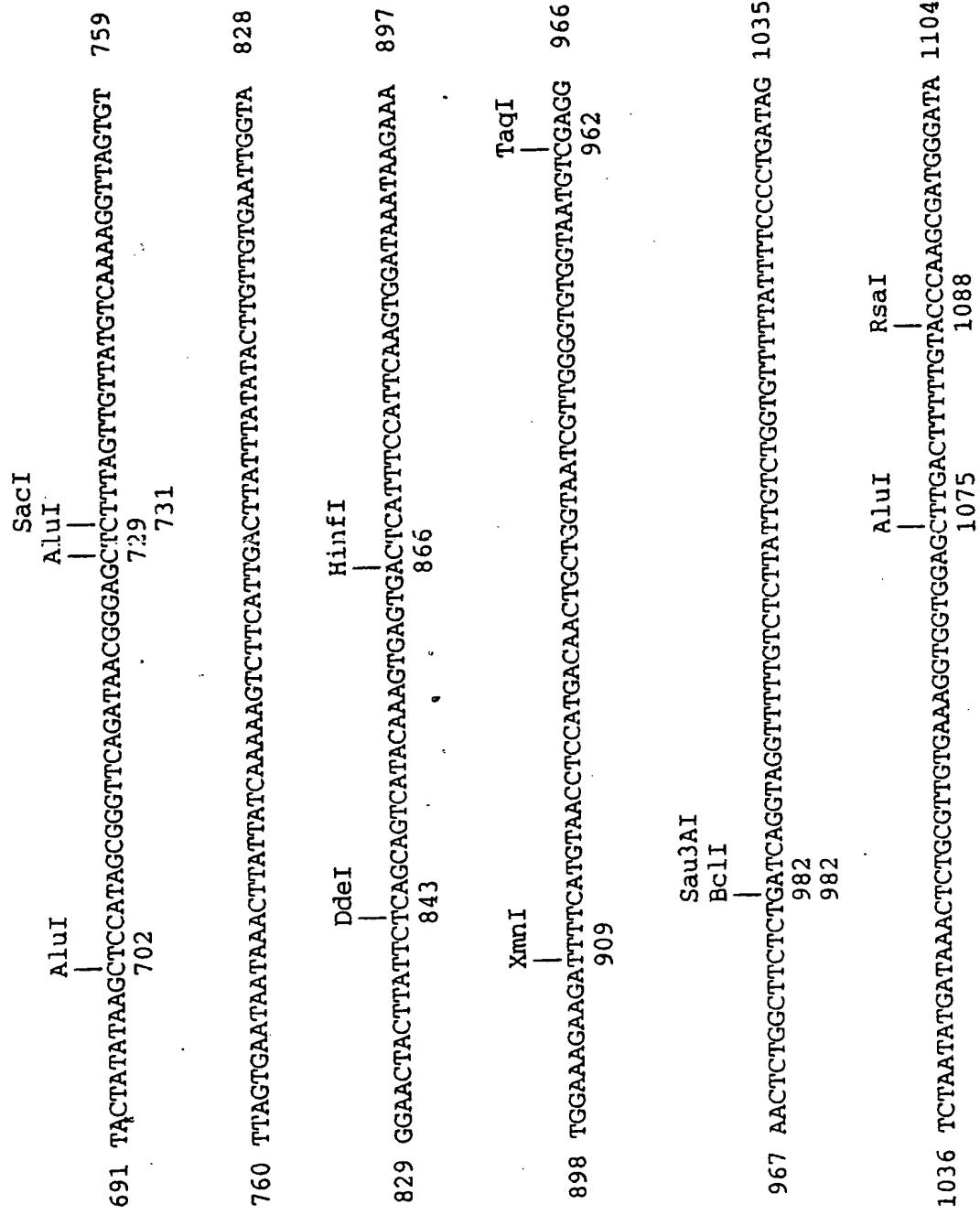


FIG. 1C

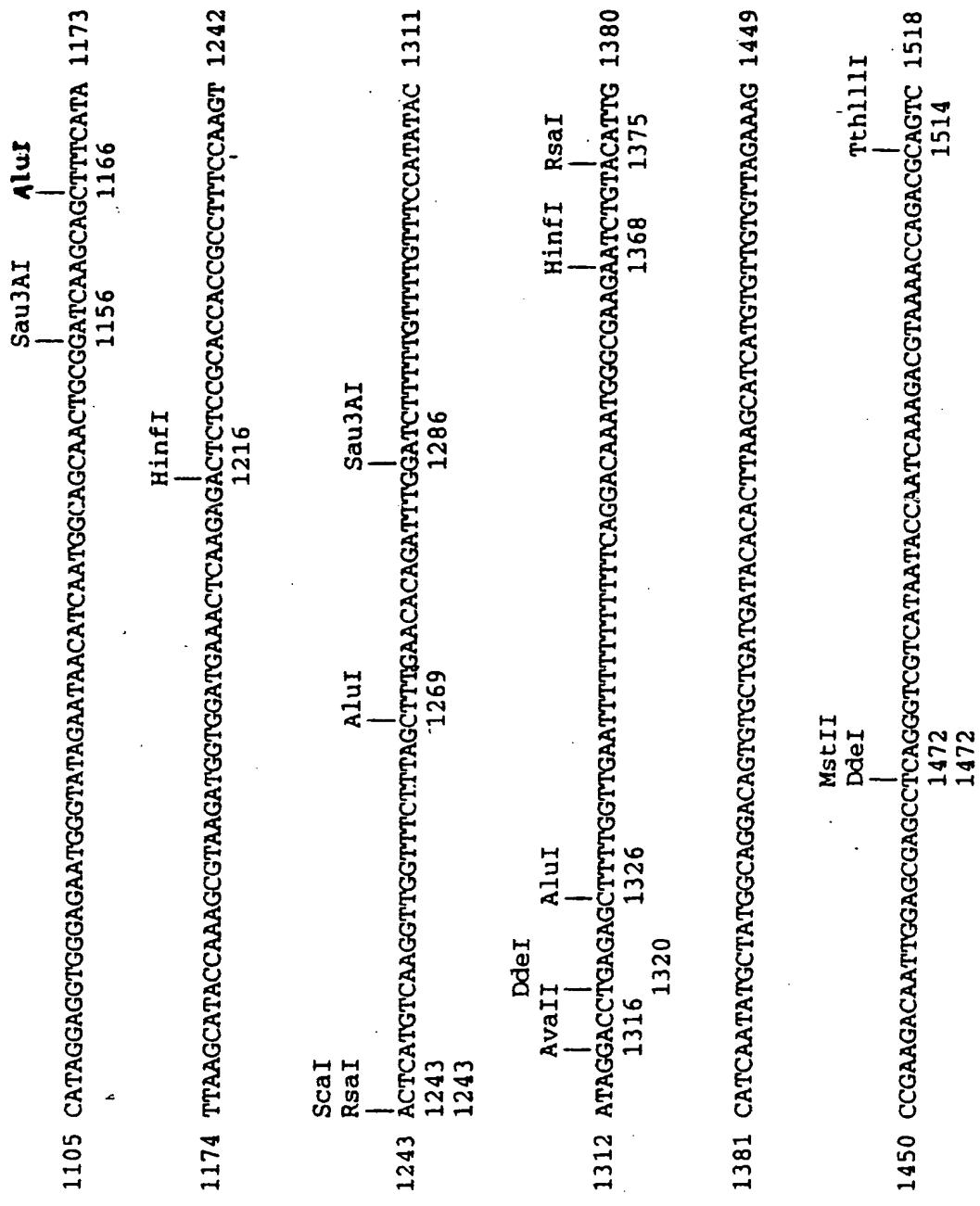


FIG. 1D

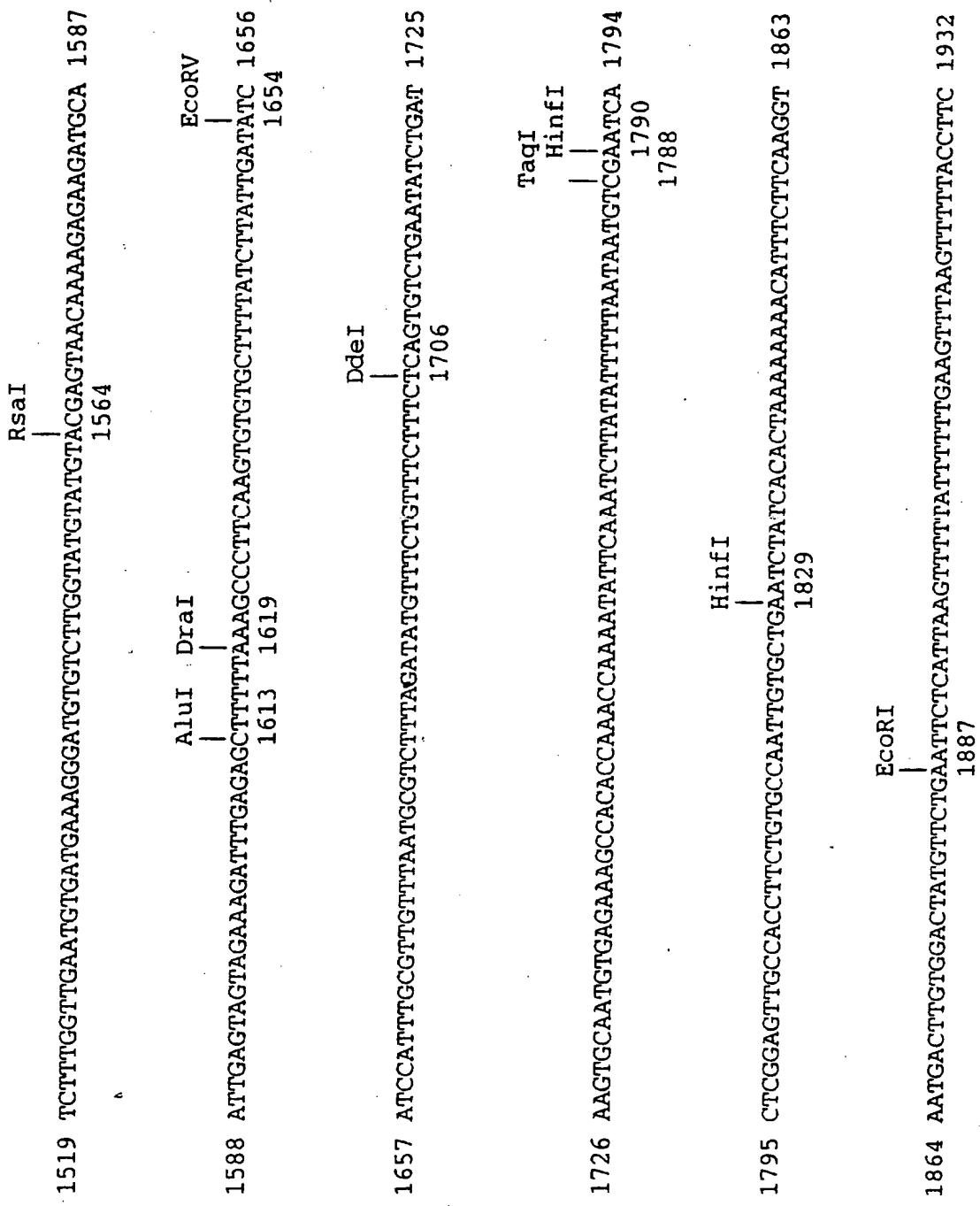


FIG. 1E

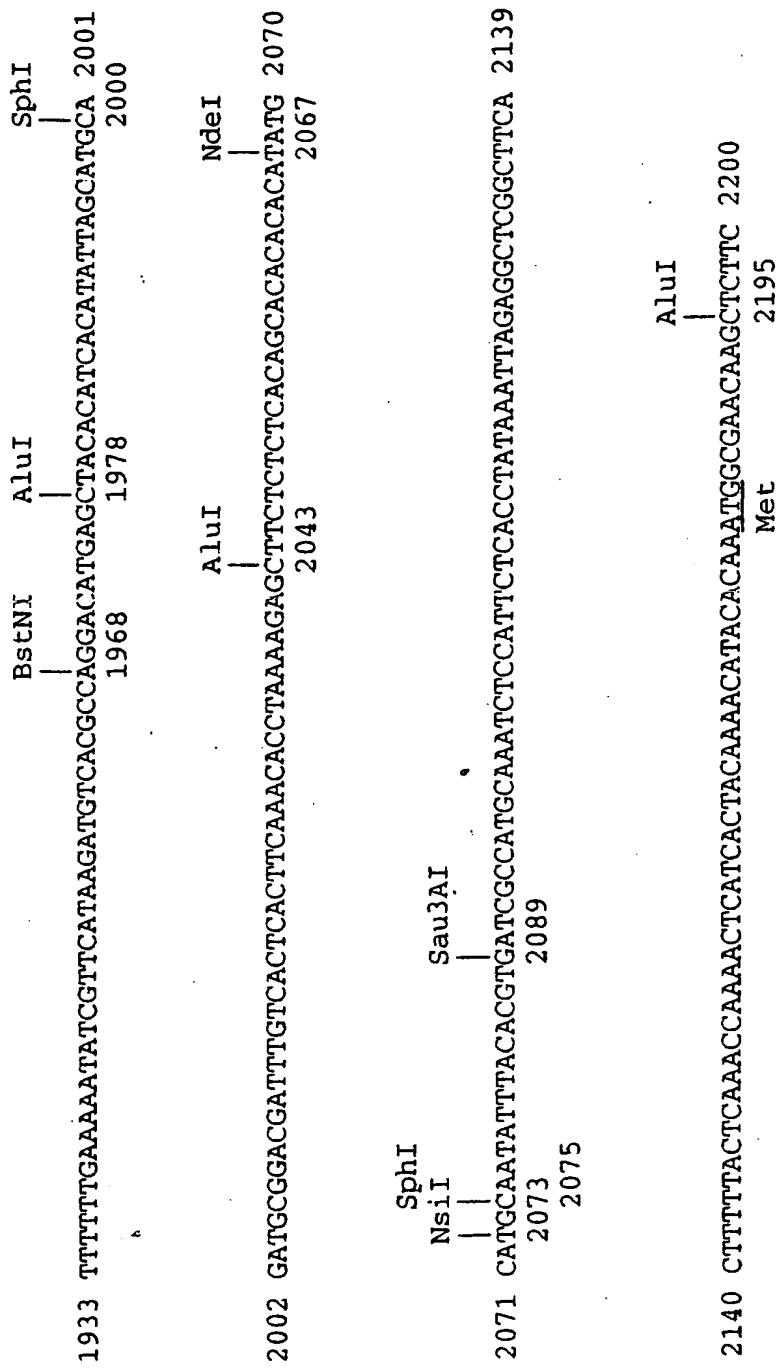


FIG. 1F

Lambda CGN1-2	LENGTH = 4325	
MCG-186 Linear		
XbaI		
TaqI		
AvaI		
1	CTCGAGGAGTCACTAACATGAAGTTGACGAGGAGCCAACTATGGAAAGCTTATTTCTCTTTGAT	69
2		
3		
HindIII		
AluI		
TaqI		
1		
2		
3		
52		
50		
66		
SacI		
AluI		
XbaI		
HhaI		
1		
2		
89		
95		
119		
121		
139	ACTCTAAATTGAGCCGTGCCTATCTAGACCAATTAGAATTGATGGAGCTCAAAAGGTCTCTTTGGATTA	138
150		
156		
171		
186		
192		
206		
207		
208	TGTTAGGGTGGCAAACCGGAAAGATTGGCTCTCAATTGGAAAGGGATGAAACGCCGAAGAAGAAA	276
223		
239		
255		
277	TAAGAAATTGGCAGTCCTGCTACTCAATGGATCTCAGCTATAACGGTCGTCATGAAACAGAGGT	345
293		
309		
305		
321		
346	AAAAACATTTTGCATAACACTTGAAGTTCCACTAACTGTTAACTCTTTGGTAGATATCACTA	414
362		
378		
394		
408		
424		
440		
456		
472		
488		
504		
520		
536		
552		
568		
584		
600		
616		
632		
648		
664		
680		
696		
712		
728		
744		
760		
776		
792		
808		
824		
840		
856		
872		
888		
904		
920		
936		
952		
968		
984		
1000		
1016		
1032		
1048		
1064		
1080		
1096		
1112		
1128		
1144		
1160		
1176		
1192		
1208		
1224		
1240		
1256		
1272		
1288		
1304		
1320		
1336		
1352		
1368		
1384		
1400		
1416		
1432		
1448		
1464		
1480		
1496		
1512		
1528		
1544		
1560		
1576		
1592		
1608		
1624		
1640		
1656		
1672		
1688		
1704		
1720		
1736		
1752		
1768		
1784		
1800		
1816		
1832		
1848		
1864		
1880		
1896		
1912		
1928		
1944		
1960		
1976		
1992		
2008		
2024		
2040		
2056		
2072		
2088		
2104		
2120		
2136		
2152		
2168		
2184		
2200		
2216		
2232		
2248		
2264		
2280		
2296		
2312		
2328		
2344		
2360		
2376		
2392		
2408		
2424		
2440		
2456		
2472		
2488		
2504		
2520		
2536		
2552		
2568		
2584		
2600		
2616		
2632		
2648		
2664		
2680		
2696		
2712		
2728		
2744		
2760		
2776		
2792		
2808		
2824		
2840		
2856		
2872		
2888		
2904		
2920		
2936		
2952		
2968		
2984		
3000		
3016		
3032		
3048		
3064		
3080		
3096		
3112		
3128		
3144		
3160		
3176		
3192		
3208		
3224		
3240		
3256		
3272		
3288		
3304		
3320		
3336		
3352		
3368		
3384		
3400		
3416		
3432		
3448		
3464		
3480		
3496		
3512		
3528		
3544		
3560		
3576		
3592		
3608		
3624		
3640		
3656		
3672		
3688		
3704		
3720		
3736		
3752		
3768		
3784		
3800		
3816		
3832		
3848		
3864		
3880		
3896		
3912		
3928		
3944		
3960		
3976		
3992		
4008		
4024		
4040		
4056		
4072		
4088		
4104		
4120		
4136		
4152		
4168		
4184		
4200		
4216		
4232		
4248		
4264		
4280		
4296		
4312		
4328		

FIG. 2A

FIG. 2B

HincII HhaII HaeII BdeI BstEII BAlI HaeIII HaeIII AluI

415 CAATGTCGAGAGACAA3GGCTGMNCANCATAACAAAAGGGAAATGAAGATGGCCTTTGATTAGCTG 483

439 438 439 439 440 438

AluI HinfI

484 TGTAGCATCAGCAGCTAACTCTGGGCTCTCATGGATGCTGGAACTGGATTCACTTCAGTTCAAGTTTA 552

498 535

MspI HpaII HinfI

553 TGAGTTGTCAACGGGCTTCCACACAAAGGTAATAATCAGTGAAGCAATTAAAGAATCAATTGATTGT 621

564 564

DdeI

622 AGTAAACCAAGAACCTACCTTATGTTTCCCCCAGGACTGGATTATGGAACATTGGAAACATTGGAAAAGAAC 690

629

AluI AluI SacI

691 TACTATATAAGCTCATAGCTGGTTCAGATAACGGGAGCTTCTTAAAGTTAGTTAATGTCAAAAGGTTAGTGT 759

702 710 729 731

760 TTAGTGAAATAAAGCTTAAACCAAAAGCTTCATTGACTTATTAACTTCTTGTGAAATTGCTAG 828
 829, GAACTACTTATTCTCAGGCACTAAACCTTCAAGCTTCAAGGGATATAAGAAAT 897
 898 GGAAGAGAAGTTTCAAGTAAACCTTCAAGACAACTGGTGTAACTTCTTCAAGGGAA 966
 967 ACCTGGCTCTCTGAGTAGGTGTTTGGCTCTTAACTGCTGGGTTTATTTCCCGGAA 966
 1036 CTAAATAAGATAAACCTGGCTTGTGAAAGGTTGGAGCTTGACTTTTGTAAAGCCAAAGGCAATGGGATAC 1104
 1105 ATAGGAGTTGGAGAAATGGGAAATAGAATAGAATAGGAGGATGAAACTCAAGAGCTCCTCCAAAGTA 1174
 1174 TAAGGATACCAAAAGCTTAAAGTGGGATGAAACTCAAGAGCTCCTCCAAAGTA 1242
 1215
 Bdel |||
 HinfI |||
 XbaI |||
 BglII |||
 SmaI |||
 SacI |||
 TaqI |||
 961
 965
 908
 842
 881
 1074
 1087
 1155 1165
 SmaI |||
 AluI |||
 SmaI |||
 AluI |||
 1173
 1242

FIG 2C

1243 CTCATGTCAGGTTGGTTCTTCTAGCTTTGAAACACAGATTGGATCTTTTGTTCATATACT 1311
 AluI | Sau3AI | PdeI |
 1268 1285 1311

1312 TAGGACCTGAGCTTTGGTTGATTTTTCAGGACAAATGGGCAAGAACATCTGACATTGCATCA 1380
 BdeI | AluI | HinfI | RsaI |
 1315 1325 1363 1370

1381 ATATGCTATGGCAGGACAGTGTCGATACACACTTAAGCATCATGTTGAAAGCCAAAGAACATTGGAG 1449
 HinfI |
 PdeI |
 1450 CGAGACTCAGGGTCGTCATAATACCAATCAAAGACGTAAACAGACGCAACCTCTTGGTGAATGTA 1518
 1454 1456

1519 ATGAAAGGGATTGGCTGGTATGTTACGATAACAAAGAGATGGAAATTAGTAGTAAATA 1587
 RsaI |
 1548

1588 TTTGGGAGCTTTTAAGCCCTCAAGTGTGCTTTATCTTATTGATATCATCCATTTCGTTGTTAA 1656
 AluI | ECORV |
 1596 1635

1657 TGGCTCTAGATAATGTCCTATATCTTCAGTGTCTGATAAGTGAATGTGAGAAACCATACCAA 1725
 XbaI | PdeI |
 1664 1687

FIG. 2D

HinfI
 1726 ACCAAATTCAAATCTTAAATTTAAATGTTGAATCACTCGGA/GTTGCCACCTCTGTGCCATTG 1794
 1761

HinfI
 1795 TGCTGAATCTACACTAGAAAAACATTCTCAAGGTAATGACTTGTGGACTATGTTCTGAATTG 1863
 1800

HinfI
 1864 TCATTAAGTTTTATTTCTGAAGTTAAAGTTTACCTCTGTGTTTGAATAATATCGTTCAAAAGATG 1932
 1933 TCACGCCAGGACATGAGCTACACATGCACATAGCATGCAGATCAGGACGATTGCACTCACTCTCAA 2001
 1940 1950 1973
 1971

BstNI
AluI
 2002 CACCTAAGGCTCTCTCACAGCCACACACATATGCATGCCATTACACGTTGATGCCATGCCAA 2070
 2006 2012 2028 2036 2042 2058
 2044

HinfI
AluI
 2071 ATCTCCATTCTCACCTATAAAATTAGAGCCTCGGCTTCACTCTTACTCAAACCAAACTCATCACTACA 2139
 2140 GAACATACACAAATGGCGAACAAAGCTCTGGCTCGGCAACTCTGGCTTCTGTTCTCTCACC 2208
 METIaAsnIyslePhelLeuIaThrLeuIaValSerIaThrLeuIaLeuPhelLeuIeLeuIhr
 2164

EcoRI
 1859

SphI
Sau3A
 1959

Bpu11
NdeI
NsiI
SphI
Sau3A
 1932

FIG. 2E

FIG. 2F

Alui

2623 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2639
2630 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2646
2631 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2652
2632 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2653
2633 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2654
2634 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2655
2635 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2656
2636 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2657
2637 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2658
2638 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2659
2639 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2660
2640 ~~AcGACTTACCTAGAGCTGGCAACATGGCA~~ 2661

2761 GTTGAGTGTAACTACATAGTCATGGGTTGTTGTTCTAAATGCTAAATGTTAATAGAAC 2829
Hinc II Rsa I

2838 TACCTGGTACGGTAAAGGAGTCTTACCTGGTACTTCCATAGGAGAT 2898
2771 Accl

FIG. 2G

FIG. 21

Brassica campestris ACP Genomic Sequence

1 AAGAGTATGCTTACTACTACTCTATAATCAAGTTCAGGAAGCTGAGCTGGCTCTCACTTATAT 69
11 46 51
47

70 GTTTGATGTTGTTGTCAGGTATGGTAAATCATGGAAAGAGATAAAGAAATGCAAACCCCTGAAGTATTGG 138

139 CAGAGAGGACTGAGGTGAGAGACATGTCACCTTTGTGTACTCATCTGAATTATCTTATAATGCGAATT 207
149

208 GTAAGTGGTACTAAAGGTTGTAACTTTGGTAGGGATTGAAGGATAATGGAGGAACCTTGCTTC 276
217

277 GCTAGGGTAAACAGTTTATATGCTATGAAGGTTTGGCTGGTACGTATCAGCAGCTGTTGGAG 345
310 338
308 338

AccI DdeI AluI AluI
| | | |
11 46 51 47

DdeI RsaI
| |
139 208 217

HindIII PvuII AluI AluI
| | | |
277 310 338 338

FIG. 3A

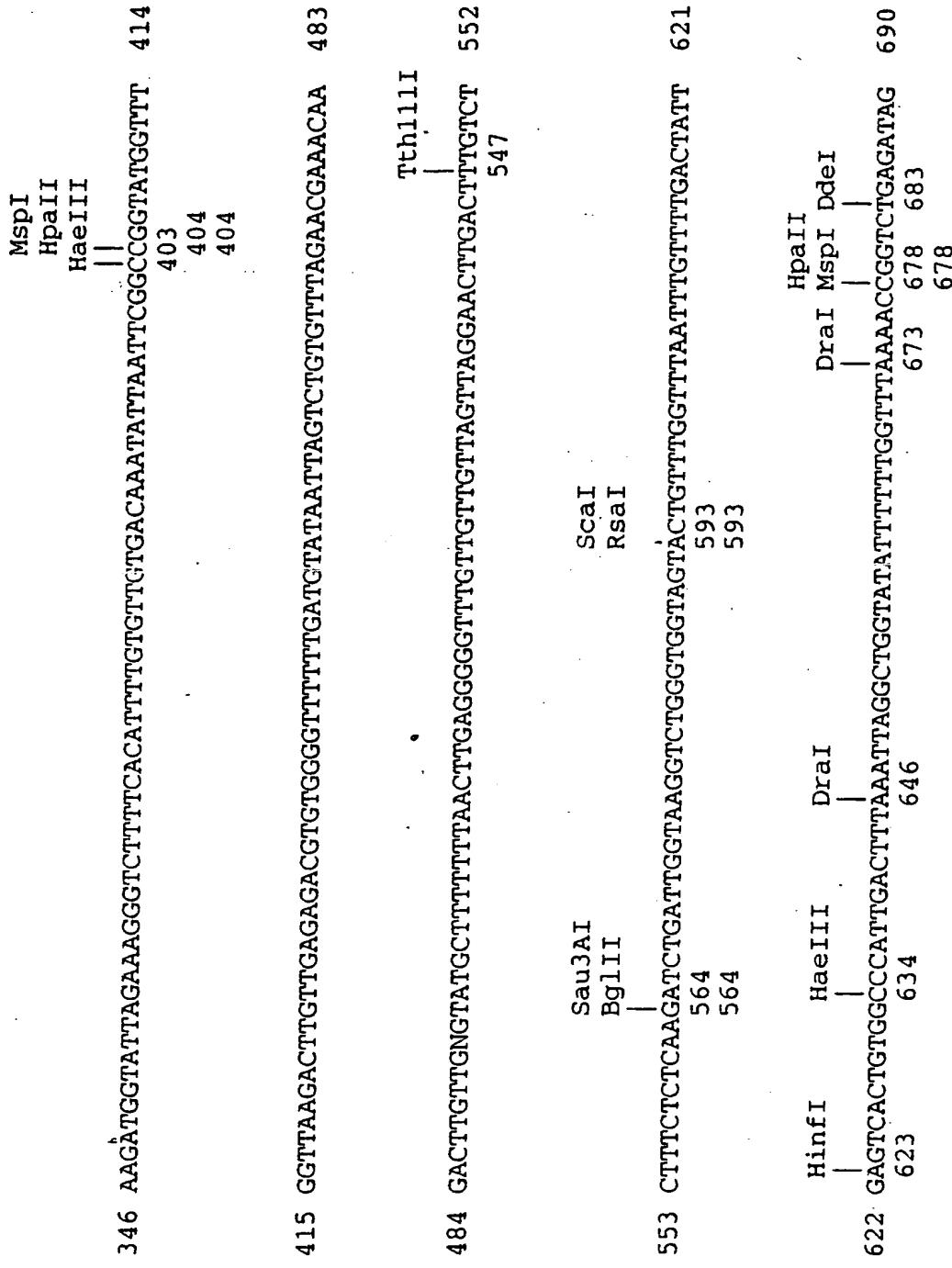


FIG. 3B

691 TGCAATTTCGATTCAGTCAATTAAATTCTTCAAGGTAATGGGCTGAATACTTGTATAGTTAAC 759

701 715 699

760 TTAACAGGCCCTTAAAGGCCATGTTATCATAAAACGTCATTGTTAGAGTGCACCAAGCTTATAAAAT 828

768 778 769

829 GTAGCCAGGCCCTTAAAGACTTAAACAGGCCCTTAAAGACTTAAACATTCCCTTAAAGGCCCATGTTATTC 897

835 838 838

898 TAAAACGTCATCGTTGAGTGCACCAAGCTTAAATGTAGCCGGCCTTAAAGACTTAAACAGGCCCTTAA 966

927 939 942 941

691 TGCAATTTCGATTCAGTCAATTAAATTCTTCAAGGTAATGGGCTGAATACTTGTATAGTTAAC 759

701 715 699

760 TTAACAGGCCCTTAAAGGCCATGTTATCATAAAACGTCATTGTTAGAGTGCACCAAGCTTATAAAAT 828

768 778 769

829 GTAGCCAGGCCCTTAAAGACTTAAACAGGCCCTTAAAGACTTAAACATTCCCTTAAAGGCCCATGTTATTC 897

835 838 838

898 TAAAACGTCATCGTTGAGTGCACCAAGCTTAAATGTAGCCGGCCTTAAAGACTTAAACAGGCCCTTAA 966

927 939 942 941

FIG. 3C

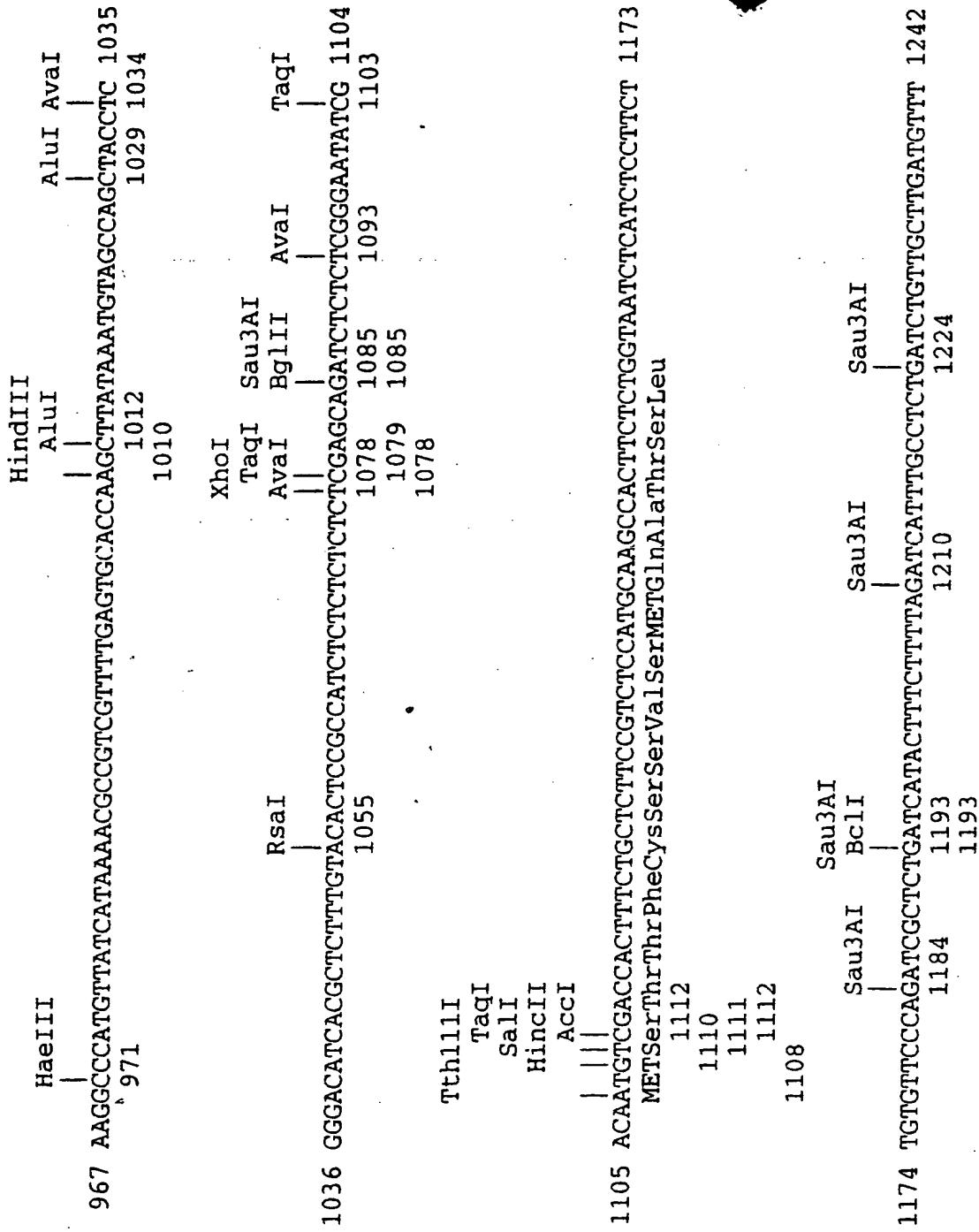


FIG. 3D

HincII | AluI | Hinfl |
 1243 GTAACTCCACGGCATGTTGATTATGTTGAGAATTAGAAAAAAATGTTAGCTTACGAAATCTTTAG 1311
 1243 1296 1303

Sau3AI | TaqI |
 BcII | Sau3AI |
 1312 TGATCATTCAATTGGATTGCAATCTTGTGTGACATTGAGGCTTGTGATTGATTCGATCTGTATTCA 1369
 1313 1368
 1313

Hinfl | AluI | DraI |
 1381 TTTGAATCACAGCTATAATAAGCTATTGAGTAGTTAGTGTGTTAAATGAACATGTTTGTGTATTGA 1449
 1386 1394 1425

AluI |
 1450 TGGAAACAAACAGGCAGCAACACGAGGATTAGTTCCAGAAGCCAGCTTGGTTCAACCGACTAAATCTC 1518
 AlaAlaThrThrArgIleSerPheGlnLysProAlaLeuValSerThrThrAsnLeu
 1496

HhaI | DdeI |
 1519 TCCTTCACACCTCCGCCGTTCAATCCCCACTCGTTCTCAATTCTCCTGGGTATGTTCTCATTTCAG 1587
 SerPheAsnLeuArgArgSerIleProThrArgPheSerIleSerCysAla
 1568 1584

FIG. 3E

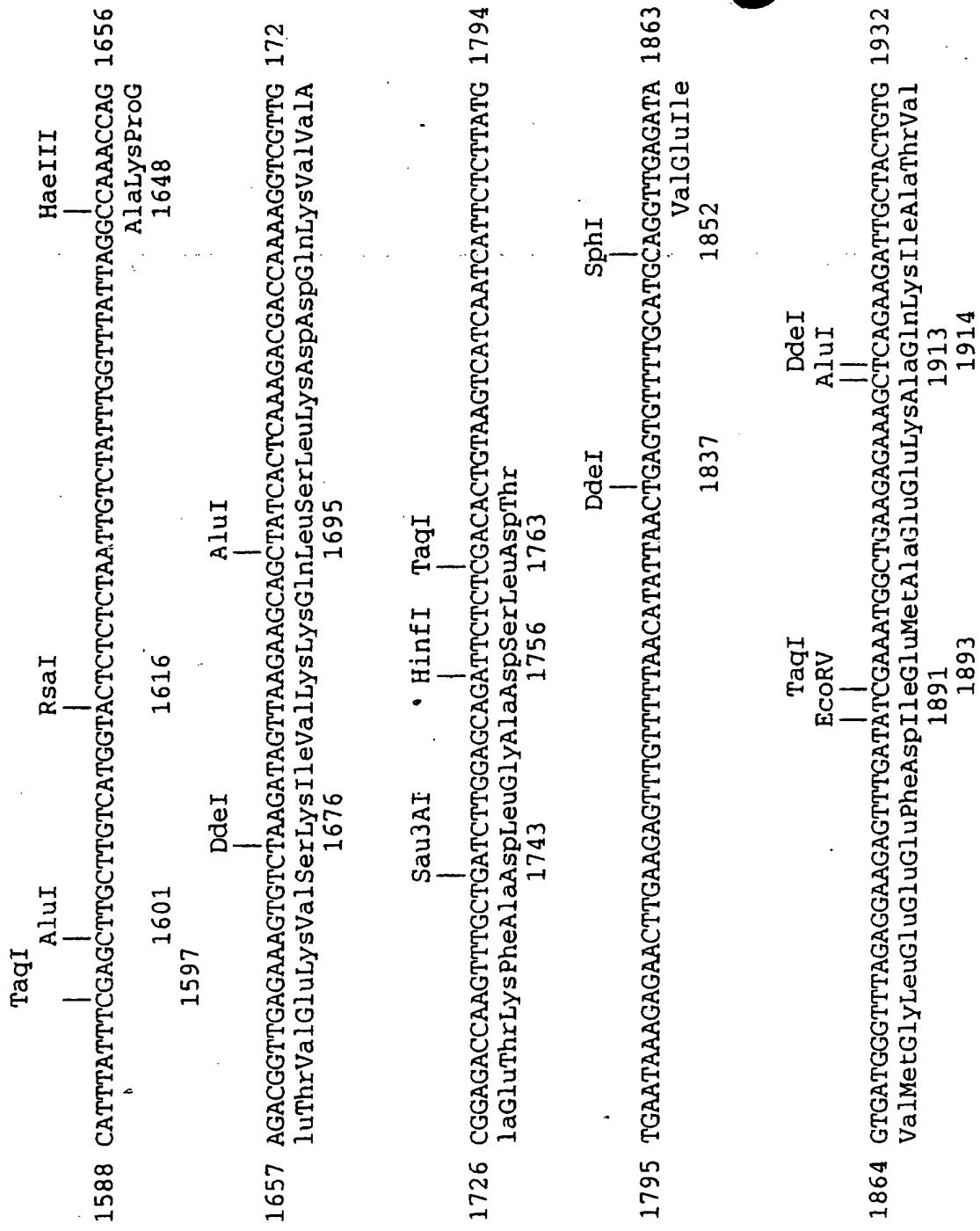


FIG. 3F

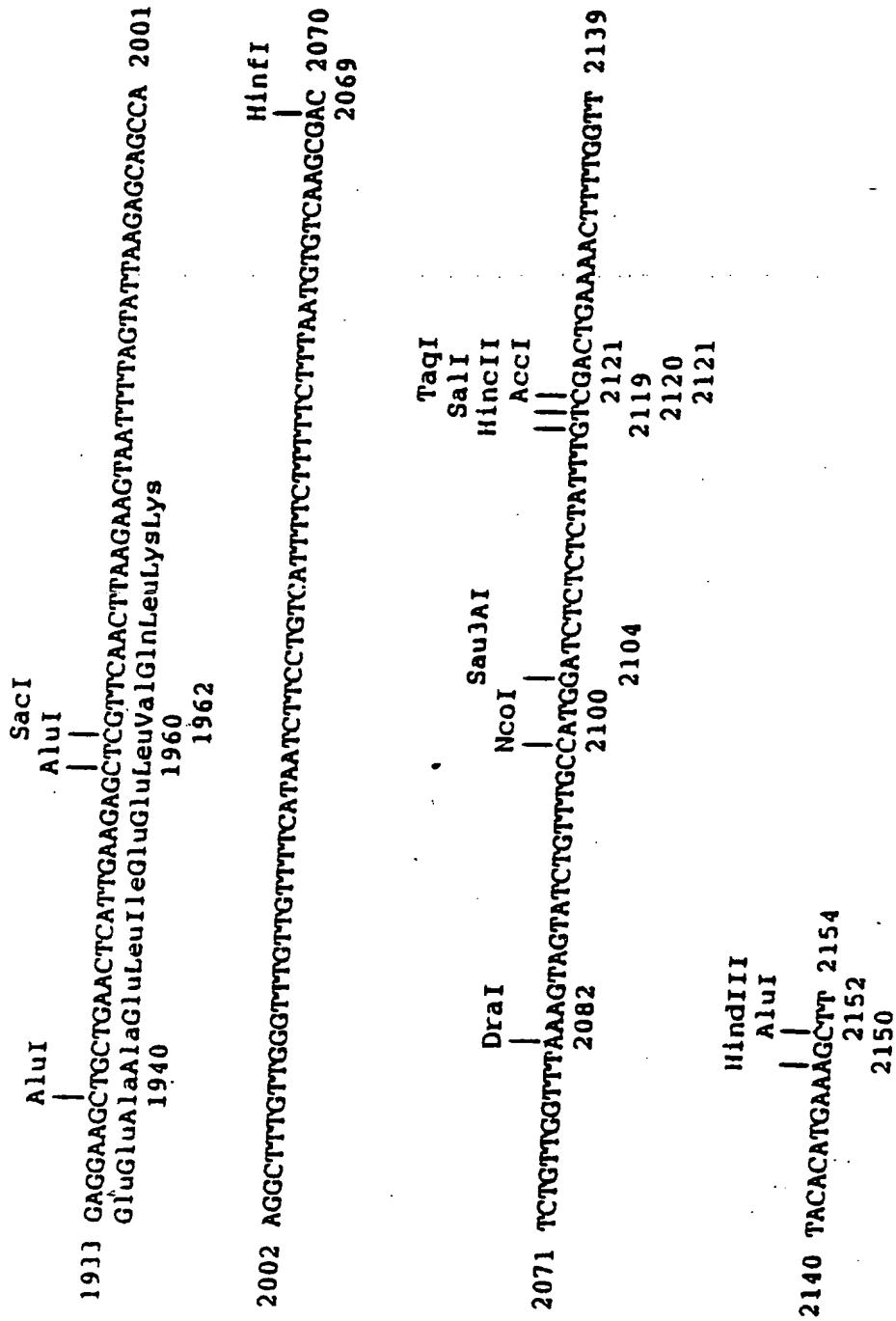


FIG. 3G

Brassica Campestris Seed Specific cDNA-EA9

Complete nucleotide sequence of *B. campestris* cDNA EA9. The longest open reading frame is designated by three letter amino acid code. PolyA tails are evident at the end of the sequence and a potential polyadenylation signal is underlined.

FIG. 4A

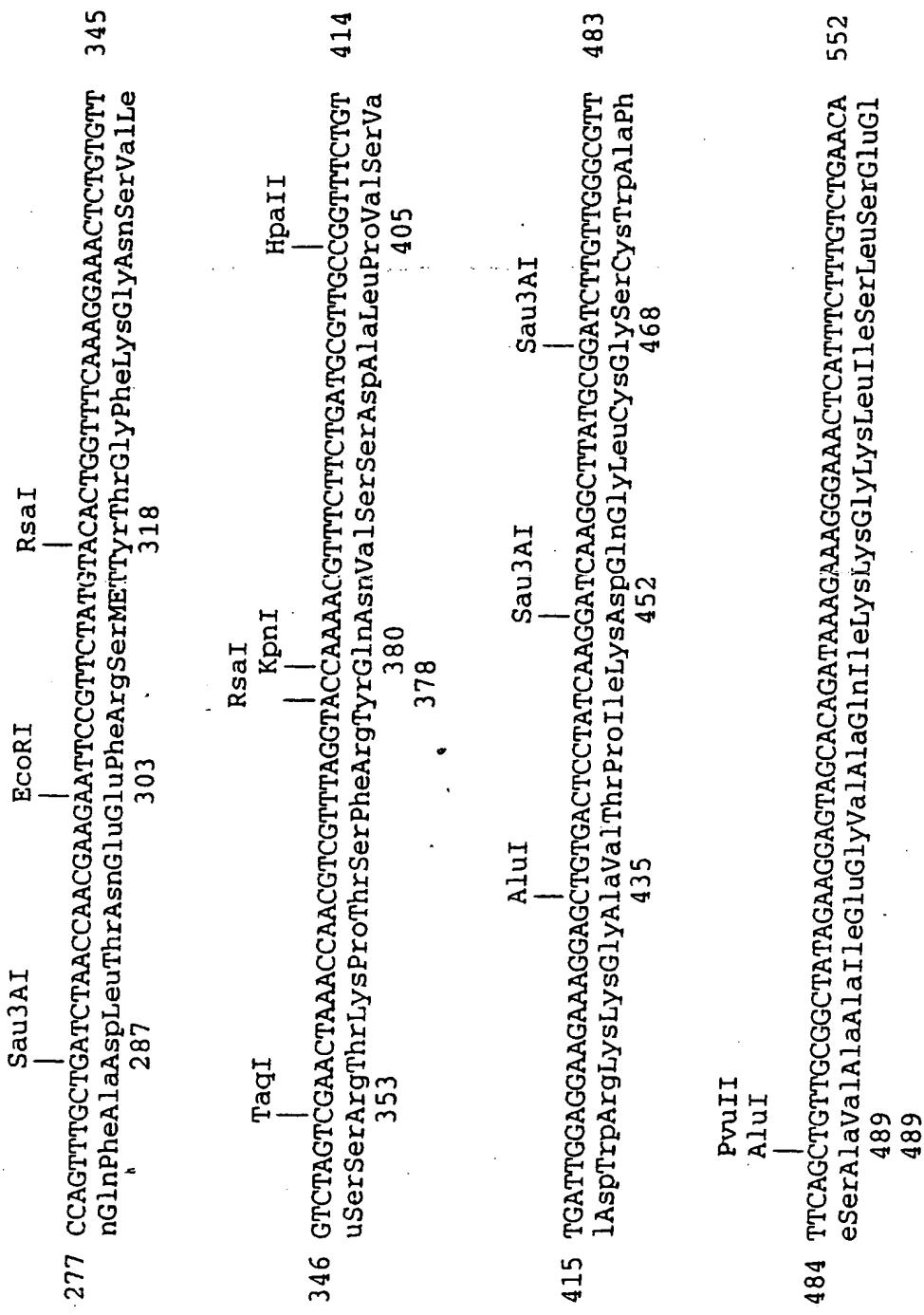


FIG. 4B

TaqI
 Sall
 HincII
 AluI AccI
 | |
 553 AGAGCTTGTGACTGGACACAAACGATGGTGGCTGCATGGCGGTTGATGGATAACAGCGTTAAC 621
 nGluLeuValAspCysAspThrAsnAspGlyGlyCysME"R1yGlyLeuMetAspThrAlaPheAsnTy
 557 562
 560
 561
 562

622 CACAAACTATTGGGGCTTAACCTCTGAAATCAAAATTATCCTTATAAAGCACAAACGGCACTTGCAA 690
 rThrIleThrIleGlyGlyLeuThrSerGluSerAsnTy_rProTy_rLysSerThrAsnGlyThrCysAS

HpaII
 |
 691 CTTCAAAACTAAACAGATAGCAACTCTATCAAAGGTTTGGGATGTCGGCTAACGATGAGAA 759
 nPheAsnLysThrLysGlnIleAlaThrSerIleAlaIleAlaGlyGlyAspIleAlaAsnAspGluIle 744

HpaII
 |
 760 AGCCCTAATGAAAGGCACTGGCACACCACCCGGTTAGGCATTGGAATAGCGGGAGGAGATATTGTTCCA 828
 SALaLeuMETLysAlaValAlaHisProValSerIleGlyIleAlaGlyGlyAspIleAlaAsnAspGluIle 789

Sau3AI
 BclI
 |
 829 ATCTATTGGTCCGGTGTTCAGCGGGAGAATGCACAAACTCATCTGATCACGGGGTAAC TGCGGTGG 897
 nPhetTy_rSerSerGlyValPheSerGlyGluCysThrThrHisLeuAspHisGlyValThrAlaValG 841
 875
 875

FIG. 4C

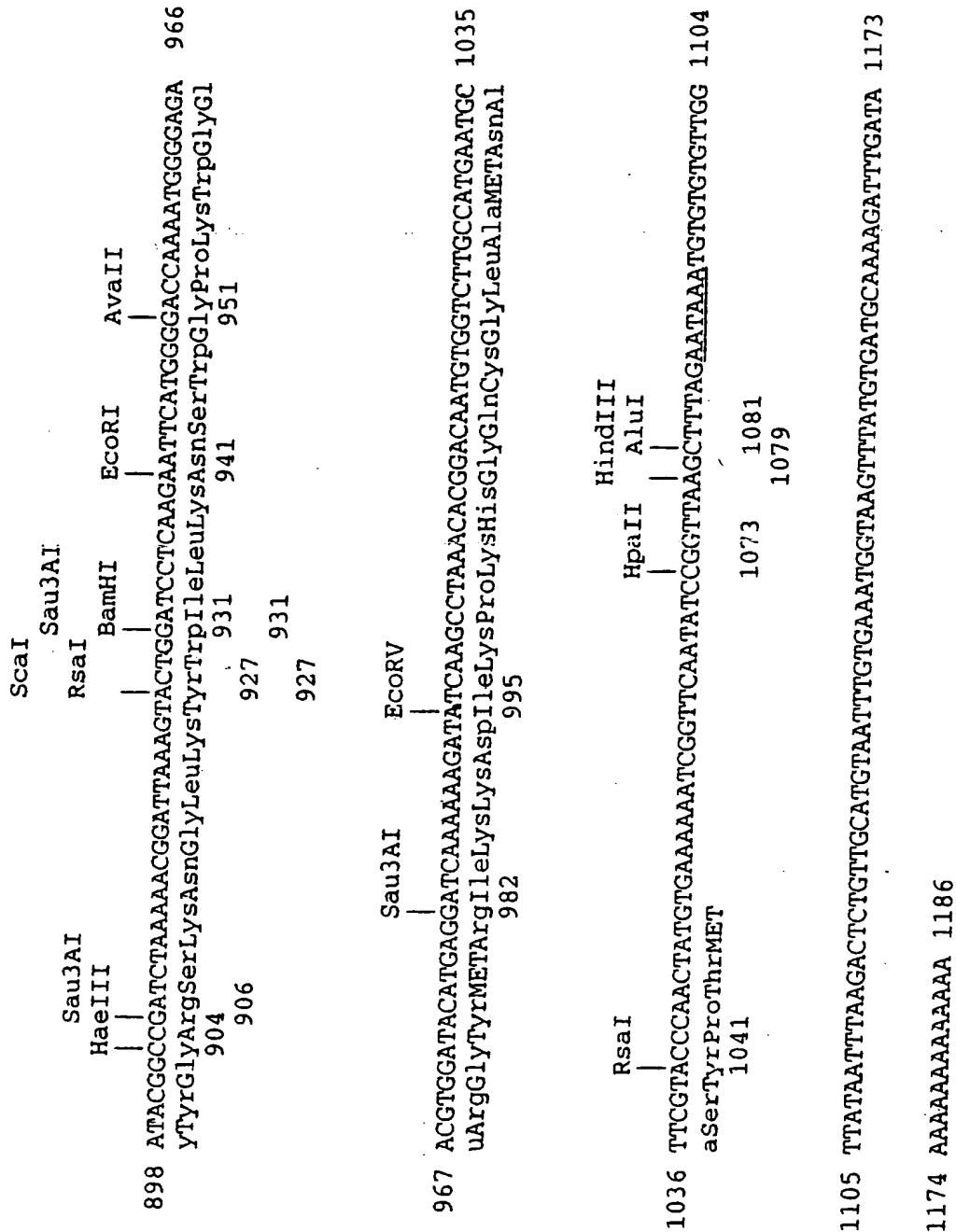


FIG. 4D

3H11 TTTTTTGAGCAAAGGGCAACTCAGATATCCAAAGATGAATCCAACATATA 51
3H11 GCTTACAGCTGGGAGAACATTGTCTAACTCTCTGAAATTAAATGTTATC 102
3H11 CAGAACCTTCATCATAAAATAATCAAAATGCAAATCTATTTTCTAC 153
3H11 TCTTGTCTAGCTTCAACTTCTTCTGCTCATCAATTAGCAATTAAATCC 204
TGCTCATCAATTAGCAATTAAATCC
3H11 AAAACCATTATGGCTGCCAAAATTCAAGAGATGAAGTTGCTATCTTCTTC 255
2A11 AAAACCATTATGGCTGCCAAAATTCAAGAGATGAAGTTGCTATCTTCTTC
METAlaAlaLysAsnSerGluMETLysPheAlaIlePhePhe
3H11 GTTGTCTTTGACGACCACTTAGTTGATATGTCCTGAAATTGAAATG 306
2A11 GTTGTCTTTGACGACCACTTAGTTGATATGTCCTGAAATTGAAATG
ValValLeuLeuThrThrLeuValAspMETSerGlyIleSerLysMET
3H11 CAAGTGATGGCTTCGAGACATACCCCCACAAGAACATTGCTGAAATG 357
2A11 CAAGTGATGGCTTCGAGACATACCCCCACAAGAACATTGCTGAAATG
GlnValMETAlaLeuArgAspIleProProGlnGluThrLeuLeuLysMET
3H11 AAGCTACTTCCCACAAATATTTGGGACTTGTAAACGAACCTGCAGCTCA 408
2A11 AAGCTACTTCCCACAAATATTTGGGACTTGTAAACGAACCTGCAGCTCA
LysLeuLeuProThrAsnIleLeuGlyLeuCysAsnGluProCysSerSer
3H11 AACTCTGATTGCATCGGAATTACCCCTTGCCTTGCCTTGCAGCTCA 459
2A11 AACTCTGATTGCATCGGAATTACCCCTTGCCTTGCCTTGCAGCTCA
AsnSerAspCysIleGlyIleThrLeuCysGlnPheCysLysGluLysThr
3H11 GACCAAGTATGGTTAACATACCGTACATGCAACCTGTTGCCTTGAACAATA 510
2A11 GACCAAGTATGGTTAACATACCGTACATGCAACCTGTTGCCTTGAACAATA
AspGlnTyrGlyLeuThrTyrArgThrCysAsnLeuLeuPro

FIGURE 5A

3H11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCGCGCTA 561
2A11 TCAATGATCTATCGATCGATCTATCTATCTATCTATTTATCTGTCTCGCGCTA

3H11 TAGTGTGTCGTACCTTGGTGTGAAGAATATGAATAAAGGGATACATAT 612
2A11 TAGTGTGTCGTACCTTGGTGTGAAGAATATGAATAAAGGGATACATAT

3H11 ATCTAGATATATTCTAGGTAAATGTCCTATTGTATTTAAAATTGTAGCAAT 663
2A11 ATCTAGATATATTCTAGGTAAATGTCCTATTGTATTTAAAATTGTAGCAAT

3H11 GATTGTTGAATAAAACATACCATGAGTGAATAATTATTCCACATTAAT 714
2A11 GATTGTTGAATAAAACATACCATGAGTGAATAATTATTCC

3H11 TCACGTATTTATTCACTTATGATACGTATTTTGTTCCTTCGCGTAAAAA 765

3H11 AAAAAAAA 774

FIGURE 5B

2A11	⑤M A L R D I P P Q E T L L
PA1b	⑤C S P F D I P P C G S P L C R C I
Chick pea inhibitor	⑤C T - K S I P P ----- Q C R C N
Lima bean inhibitor	L C T - K S I P P ----- Q C R C T
α_1 -antitrypsin	L G A I P M S I P P E V

2A11	T N I L G L C N E P C S S N S D C I
PA1b	G S P L C R C I P A G L V I G N C R
Barley chloroform/ methanol-soluble protein d	T N L L G N C R - F Y L V Q Q T C A
Wheat α -amylase inhibitor 0.28	V S A L T G C R - A M V K L Q C V
Wheat albumin	V P A L P A C R P L - L R L Q - C N
Millet bi-functional inhibitor	N N P L D S C R W Y V S A T K R . T A C G
Castor bean 2S small subunit	Q Q N L R Q C Q E Y I K Q Q V S G Q
Napin small subunit	A Q N L R A C Q Q W L N K Q A M Q S

FIGURE 6

2A11 GENOMIC

	10	20	30	40	50
CTCGAGCCCT	TTAAAAAGTA	TAGTCAATAT	TTACGGTGAC	CGTGAATTTC	
60	70	80	90	100	
TTAATTATGA	TATATAATTT	AAAAGAAATC	ATGATCACAT	TCTACTGATG	
110	120	130	140	150	
AGAACATGTG	CTAATCAAGG	GAAAACATGG	ATGTGAAAAAA	TACTTTTGT	
160	170	180	190	200	
TAAAAGTAAA	AAAAAAATGTG	AAATTTGTT	AGTTATTTAC	TACCTATACA	
210	220	230	240	250	
TTATTTGAGC	ATGTGCAAAC	TTTACAAATA	CCTAATAGAA	GATTTTCACC	
260	270	280	290	300	
TGCCTGTATA	TATGTAAATT	AATTATAATG	AACACTCTCA	CATAAAATAA	
310	320	330	340	350	
TTATCAGTAT	ATACATTAAT	ACTTGCCCTC	CACAATGAAT	TAAATAAAAT	
360	370	380	390	400	
GTAGAACATG	ATCTACACTT	CAATAAAACT	AAGACCATAA	AGAATAATTT	
410	420	430	440	450	
CAAAATATAC	ACATGTCAAC	AATAAATTAT	TTGCATATTA	TATTAACTTA	
460	470	480	490	500	
CTAAACAATC	TTTACTTTG	AAATATAAAA	ATAATCAAGT	TATAAGTCTG	
510	520	530	540	550	
CTCAAAGTAA	AGCACTTGTT	AGACTCATCT	GATTTGAGA	AGGTAAGCAA	
560	570	580	590	600	
ATTGATGGTG	CATAATAGTC	ACAAGTAAAA	TATAAAATAG	ATTCATTAG	
610	620	630	640	650	
TAAAATTGTT	TTTTACTTTC	TTTATATATA	ATTATCAATA	TCCTTCAATG	
660	670	680	690	700	
GTAGGTTAAT	TATATTGTTA	ACTTCTTGT	GAATTAAAGC	AATAAGACAA	
710	720	730	740	750	
GAATATTAAA	GATAAAAGAA	CAATAAAAAT	AGAAAGACTA	AGAGATAAGA	
760	770	780	790	800	
GTTTCTTAT	TCTTCTTCA	ATAAGTATCA	TCAAGTGTAT	ACAATATAAA	
810	820	830	840	850	
TTTTGTATT	TTTGATCTAT	CTATTTATAA	TGTTATATAT	AAGCATAACAA	
860	870	880	890	900	
AAGATCAGTC	ATAAATATGA	CTTTAATCAT	GAAAATAATG	AAAGAGATTA	
910	920	930	940	950	
TGAAGGCGTA	AGGTTACTAG	AATAATAGTC	ATTAAAAAAA	GGGGTTATCT	
960	970	980	990	1000	
TTATAATTGA	ATAATTGATG	AAGTAATGGA	GATAATTAGT	GAGCATAAAT	
1010	1020	1030	1040	1050	
TTTTTAAAAA	AAATGGACAT	TTACACTATA	ATATTTATA	ACACTTTCCC	
1060	1070	1080	1090	1100	
TTAAACATCT	AGGTATAAAAT	AATGAGTCTT	GTCAAAATCT	TAGTAGGAAA	

FIGURE 7A

1110	1120	1130	1140	1150
AATTCTGTGA	AATTTTTTA	GTGAAAACAA	ATGATATAAAA	TATCTTGAAT
1160	1170	1180	1190	1200
ACTCATATT	TGTTGCTCA	TTAAAAATCT	TATCTGACCT	ATAAAATAAA
1210	1220	1230	1240	1250
TTATTTGCTC	AACTCAAAAT	AGTTTTCAT	TCTAAAATTA	GTATAATTAT
1260	1270	1280	1290	1300
TAGTGAATAT	TTAATTAACA	TAATTGTATA	CTAAGGGGCC	TATAAATTGG
1310	1320	1330	1340	1350
ATTCTTCTCA	AAGAAAAATA	AAATCACCAC	ACAACTTTCT	TCTTCTGCTC
1360	1370	1381	1390	
ATCAATTAGC	AATTAATCCA	AAACCATT	ATG GCT GCC AAA AAT	
			MET Ala Ala Lys Asn	
1399	1408	1417	1426	
TCA GAG ATG AAG TTT GCT ATC TTC TTC GTT GTT CTT TTG				
Ser Glu MET Lys Phe Ala Ile Phe Phe Val Val Leu Leu				
1435	1444	1454	1464	1474
ACG ACC ACT TTA GGTCACAAAC	ACTTCTCCCT	TATTTGTTT		
Thr Thr Thr Leu				
1484	1494	1504	1514	1524
TCTTAATTTC	TTGGAAGTCA	TATGCATGTG	TTTGGTATCA	TGGTATATAT
1534	1544	1554	1564	1574
ATAAAGGAAA	ATATTTTCT	TAATTACTGG	TTTTCTAATG	TTTGGTAGGT
1584	1594	1604	1614	1624
AATCGGAAAT	TATTATGAGA	TAATGAACCT	GCAAAGTCAT	TATTATATAA
1634	1644	1654	1664	1674
CTTTTTTTT	ATACTTTGAT	TTAAGAATTC	TTTTTCTCA	TTTTATATAA
1684	1694	1704	1714	1724
ACTTATTTT	CAACAGAAAA	TATTTTCGA	ACTATTCAAA	CACACCCCTAA
1734	1744	1754	1764	1774
GACATTACAT	ATATATATAT	ATACACCCCTC	CGTTTATAT	TACTTAATGC
1784	1794	1804	1814	1824
CTATTGAGTT	GGCCCACCCCT	TTAAGAATGA	TTCAATTAGA	GATATGTTT
1834	1844	1854	1864	1874
ACTAAATTAA	CCTATGCTTT	AAGACTCTAA	ATTTGGCTAT	TACTATTTA
1884	1894	1904	1914	1924
CGTTGTAATT	TAATGACAAA	CATTTCATAA	TGACTATAGT	CTGAACCTAA
1934	1944	1954	1964	1974
TTAGACAGAC	GTATCTATAG	TTTGCTTACT	AATGATTCTAT	AGCTATATAT
1984	1994	2004	2014	2024
TTGGAGAGGA	GAGAGACAAA	CGATATTAAG	AAAGGGAGGA	GAGAGGCGAG
2034	2044	2054	2064	2074
GTAAATCTGA	AATAGAGAAG	AGAAAGGCAA	CCAATTTGA	TCATCTATCA
2084	2094	2104	2114	2124
TACTTTGAT	TATTATTTT	ATTATATGTA	CGTTTACATT	ACAGTTTCG

FIGURE 7B

2134	2144	2154	2164
AATTCTTACA TTAATCTTAA TCATAATATA TACA GTT GAT ATG			
		Val	Asp MET
2173	2182	2191	2200
TCT GGA ATT TCG AAA ATG CAA GTG ATG GCT CTT CGA GAC			
Ser Gly Ile Ser Lys MET Gln Val MET Ala Leu Arg Asp			
2209	2218	2227	2236
ATA CCC CCA CAA GAA ACA TTG CTG AAA ATG AAG CTA CTT			
Ile Pro Pro Gln Glu Thr Leu Leu Lys MET Lys Leu Leu			
2254	2263	2272	2281
CCC ACA AAT ATT TTG GGA CTT TGT AAC GAA CCT TGC AGC			
Pro Thr Asn Ile Leu Gly Leu Cys Asn Glu Pro Cys Ser			
2290	2299	2308	2317
TCA AAC TCT GAT TGC ATC GGA ATT ACC CTT TGC CAA TTT			
Ser Asn Ser Asp Cys Ile Gly Ile Thr Leu Cys Gln Phe			
2326	2335	2344	2353
TGT AAG GAG AAG ACG GAC CAG TAT GGT TTA ACA TAC CGT			
Cys Lys Glu Lys Thr Asp Gln Tyr Gly Leu Thr Tyr Arg			
2371	2380	2393	2403
ACA TGC AAC CTG TTG CCT TGA ACAATATCAA TGATCTATCG			
Thr Cys Asn Leu Leu Pro			
2413	2423	2433	2443
ATCGATCTAT CTATCTATT ATCTGTCTCT GCGCGTATAG TGGTGTCTGT			
2463	2473	2483	2493
ACCTTTGGTG TGAAGAATAT GAATAAAAGGG ATACATATAT CTAGATATAT			
2513	2523	2533	2543
TCTAGGTAAT GTCCTATTGT ATTTAAAATT TGTAGCAATG ATTGTTGAA			
2563	2573	2583	2593
TAAAAAACATA CCATGAGTGA AATAATTATT CCACATTAAT TCACGTATTT			
2613	2623	2633	2643
ATTTCACTTA TGATACGTAT TTTTGTTCCT TTTCGCGTAGA TTTTGATCC			
2663	2673	2683	2693
TTTTCCCTTT TGAATATTAA ACATTAACAA CAAATAATGT TTATTAAATT			
2713	2723	2733	2743
AAGTTAATAT TTTTATTAG CTATTTATAT TTTTATTGAA AATCAAACCTT			
2763	2773	2783	2793
GATAAAATATT TATAAAGATA ATTAACAAGT AATGTGACAC TAACACCATG			
2813	2823	2833	2843
TAATATTATC TTGTCGTTAT TTATGATAAT ATTTAAAAT TATAATTCA			
2863	2873	2883	2893
GTTAAAAAAAT TATTAACAAA ACATACTTTT AAAAAGTGAG TTAGCCTCCG			
2913	2923	2933	2943
CTACCCACAT ACTTATGAAT TGGACTAGTT GTTTTTGAC CCACAAAAAG			
2963	2973	2983	2993
AATGGGCTAA TTAAACCTGA CCTATCAAAT TTCAGAATCT GCATAGATTA			

FIGURE 7C

3013	3023	3033	3043	3053
GTCCGAACGA	AATGAGTCAG	CCCGTATTGA	ACAAAATATC	AACAAGGACG
3063	3073	3083	3093	3103
TTATGTAAAG	ATGTTAAGA	AGGAAAAAAAG	ATTTCTAATA	CATATGGACT
3113	3123	3133	3143	3153
TTCAATATCC	CAACTTGTC	TGGCGATCTG	AACCCTGCTT	AGTTTGTGAA
3163	3173	3183	3193	3203
TCATTAACCT	GTCTTGCTAT	GTATTTAAGA	TTTAAACTT	ATATGTTAA
3213	3223	3233	3243	3253
ACTTACAGAA	AATACATATA	AATCTCTCAA	GACTTGGCAA	CATAATTTAC
3263	3273	3283	3293	3303
TTTAGTACTT	AAACTACATG	AAAATTAAA	TATCCTTTA	ACATCTTGAA
3313	3323	3333	3343	3353
AGTGAATTAA	ATTATCACAA	TCCGAGCCTA	CACCTTGGAC	GTGGCCGGCA
3363	3373	3383	3393	3403
CTCAAGAACCC	AGTGCTGGTC	CCCAAGCTAA	CCCTCATCCT	GACTGACTAC
3413	3423	3433	3443	3453
AAGCGGAAGG	CTAACCTAAG	TATACAAAAG	CTTAAAACG	AATAAAATAA
3463	3473	3483	3493	3503
ACTTTACAAG	GTTTTAACAC	AAATGAACAA	CTTTGAAGAA	AATAATATAT
3513	3523	3533	3543	3553
TCAACTAGCC	ATAAAATAGA	CAACTTTAGT	CTTTAAAACA	TTTAATAAAA
3563	3573	3583	3593	3603
TAAATGCAA	ATATAGACTC	CTTAACTAAA	CTGACTATCT	ATGGAGCCTC
3613	3623	3633	3643	3653
TAATTGATAA	AGATGGAAGT	CGGGACAAAGA	CCACGACATC	CTGACTAAAC
3663	3673	3683	3693	3703
TGAGAAGTAA	ATAAAATCCC	CCGGAAAAAA	AGGAGCCTCA	CCATGGCTAA
3713	3723	3733	3743	3753
CTCGAACTCG	GGGATATATC	AATGAAGCTC	CTGTTGATGA	TCTTGAAGAC
3763	3773	3783	3793	3803
ATGTCTCTGC	ATCATAAAAA	AGATGCAGGC	CAAATGGCTC	AGTACGTAAA
3813	3823	3833	3843	3853
ATGTACGAGT	ATGTAAGGGA	AATTCTAAAG	TATAACATAA	GCTTGATACT
3863	3873	3883	3893	3903
TGAATAAAAG	GAAACATACT	TACCTCTTT	CAACTCAACT	CAAATTAAGA
3913	3923	3933	3943	3953
ATAAGATACT	CAACTCAAAG	ATTAGGTATT	CAACGCAAAT	ATGGCACTCT
3963	3973	3983	3993	4003
ACTCAATGAA	GTACAAATTA	ACTCAGGATA	CTCGACTTAA	GATACTCAAC
4013	4023	4033	4043	4053
TCCCGACACT	CAACTGAACT	CATTTCAATA	TAAAGCAGCT	AAAACAAGT
4063	4073	4083	4093	4103
TCAGTATAAA	GTAAAGTTGT	TTAAAAACAT	GATGTCAACT	CTGTGTGTAT
4113	4123	4133	4143	4153
AATAAGGGAT	ACAAACATAAC	TTTGAAATGT	ATATAAAAAT	ACAATTAAC

FIGURE 7D

4163	4173	4183	4193	4203
GATGTATATA	AAAATACATT	AATCTATGGG	AGATTCTCTA	ACCGACAAACC
4213	4223	4233	4243	4253
ATCACTTAAG	GGCTAAGATG	ATGATATAGC	GATCTACCGC	ACGCTGCCAT
4263	4273	4283	4293	4303
CGCATCTTAT	ACCCGGCCAA	AGGTATAAGA	CCTGAACCTGC	CTAATGAATC
4313	4323	4333	4343	4353
CACTAATAAA	CTGTTAAAAG	GAATCATCTA	AAAAGTATGA	CCCTTTCTA
4363	4373	4383	4393	4403
CCCATAGTGG	CTAACATGGT	TTATGGGGC	TGTGAGTTAT	CTGAACCTCTC
4413	4423	4433	4443	4453
CCCCATATCG	GTGCTCAATA	CTACTCCAAA	AAATATACTG	CTCTTATGTT
4463	4473	4483	4493	4503
TAAAAACATA	CTGATTCTGT	GGTTTGAAAT	TATTGCTTAA	AGCTTAGATT
4513	4523	4533	4543	4553
TTTGAAAAGC	TCTCTTTGA	AAATCGTAGT	TTCCTTTTC	TTCTATTAAA
4563	4573	4583	4593	4603
GCTAGACATA	GGCTATGTAG	AACTCTAGCT	TACCTTCCTT	CTCAAAAGTT
4613	4623	4633	4643	4653
TGAAAACATT	TGCTTAGATT	CTTAGGGACT	ACTTAGTTCC	CTTGTGGAA
	TTC			

FIGURE 7E

PG GENOMIC

10 20 30 40 50
AAGCTTCTTA AAAAGGCAAA TTGATTAATT TGAAGTCAAA ATAATTAATT

60 70 80 90 100
ATAACAGTGG TAAAGCACCT TAAGAAACCA TAGTTGAAA GGTTACCAAT

110 120 130 140 150
GCGCTATATA TTAATCAACT TGATAATATA AAAAAAATTGTTT CAATTGAAA

160 170 180 190 200
AGGGCCTAAA ATATTCTCAA AGTATTGAA ATGGTACAAA ACTACCATCC

210 220 230 240 250
GTCCACCTAT TGACTCCAAA ATAAAATTAT TATCCACCTT TGAGTTTAAA

260 270 280 290 300
ATTGACTACT TATATAACAA TTCTAAATTGTTT AAACTATTGTTT AATACTTTA

310 320 330 340 350
AAAATACATG GCGTTCAAAT ATTTAATATA ATTTAATTGTTT TGAATATCAT

360 370 380 390 400
TTATAAACCA ACCAACTACC AACTCATTAA TCATTAATTC CCACCCAAAT

410 420 430 440 450
TCTACTATCA AAATTGTCCT AAACACTACT AAAACAAGAC GAAATTGTTG

460 470 480 490 500
GAGTCCGAAT CGAACGACCA ATCTAATTGTTT GGTTGAGCCG CATATTTAGG

510 520 530 540 550
AGGACACTTT CAATAGTATT TTTTCAAGC ATGAATTGAA AATTAAAGAT

560 570 580 590 600
TAATGGTAAA GAAGTAGTAC ATCCCGAATT AATTCAATGCC TTTTTTAAAT

610 620 630 640 650
ATAATTATAT AAATATTGTTT GATTGTTTAA AATATTAAA ACTTGAATAT

660 670 680 690 700
ATTATTTTTT TAAAAAATTAT CTATTAAGTA CCATCACATA ATTGAGACGA

710 720 730 740 750
AGGAATAATT AAGATGAACA TAGTGTAA TAGTAATGG ATGGGTAGTA

FIGURE 8A

760 770 780 790 800
 AATTTATTAA TAAATTATAT CAATAAGTTA AATTATAACA AATATTTGAG
 810 820 830 840 850
 CGCCATGTAT TTTAAAAAAAT ATTAAATAGT TTGAATTAA ACCGTTAGA
 860 870 880 890 900
 TAAATGGTCA ATTTGAACC CAAAAGTGGA TGAGAAGGGT ATTTAGAGC
 910 920 930 940 950
 CAATAGGRGG ATGAGAAGGA TATTTGAAG CCAATATGTG ATGGATGAAG
 960 970 980 990 1000
 GATAATTTG TATCATTCT AATACTTAA AGATATTTA GGTCACTTC
 1010 1020 1030 1040 1050
 CCTTCTTAG TTTATAGACT ATAGTGTAG TTCATCGAAT ATCATCTATT
 1060 1070 1080 1090 1100
 ATTTCCGTCT TAAATTATTT TTTATTTAT AAATTTTTA AAAATAAATT
 1110 1120 1130 1140 1150
 ATTTTTCCA TTTAACTTTG ATTGTAATTA ATTTTAAAA ATTACCAAACA
 1160 1170 1180 1190 1200
 TATAAATAAA ATTAATATTT AACAAAGAAT TGTAACATAA TATTTTTTA
 1210 1220 1230 1240 1250
 ATTATTCAAA ATAAATATTT TTAAACATCA TATAAAAGAA ATACGACAAA
 1260 1270 1280 1290 1300
 AAAATTGAGA CGGGAGAAGA CAAGCCAGAC AAAAATGTCC AAGAAACTCT
 1310 1320 1330 1340 1350
 TTCGTCTAAA TATCTCTCAT CCAAACTAAT ATAATACCCA TTATAATTAA
 1360 1370 1380 1390 1400
 CCATATTGAC CAACTCAAAC CCCTTAAAAT CTATAAATAG ACAAAACCTT
 1410 1420 1430 1440 1450
 CCCATACCTC TTATCATAAA AAAAATAATA ATCTTTTCA ATAGACAAGT
 1460 1470 1480 1490 1500
 TTAAAAACCA TACCATATAA CAATATATCA TGGTTATCCA AAGGAATAGT

FIGURE 8B

1510	1520	1530	1540	1550
ATTCTCCTTC	TCATTATTAT	TTTGCTTCA	TCAATTCAA	CTTGTAGAAG
1560	1570	1580	1590	1600
CAATGTTATT	GATGACAATT	TATTCAAACA	AGTTTATGAT	AATATTCTTG
1610	1620	1630	1640	1650
AACAAGAATT	TGCTCATGAT	TTTCAAGCTT	ATCTTTCTTA	TTTGAGCAAA
1660	1670	1680	1690	1700
AATATTGAAA	GCAACAATAA	TATTGACAAG	GTTGATAAAA	ATGGGATTAA
1710	1720	1730	1740	1750
AGTGATTAAT	GTACTTAGCT	TTGGAGCTAA	GGGTGATGGA	AAAACATATG
1760	1770	1780	1790	1800
ATAATATTGT	AAGTATTAA	ATATTGGAAT	ATATTTGTGG	GGATGAAAAT
1810	1820	1830	1840	1850
GATAGAGAAT	ATAAGAATTA	TTTGGAAAGGA	TGAAAAGTTA	TATTTTATAA
1860	1870	1880	1890	1900
AGTAGAAAAT	TATTTTCTCG	TTTTTAGTAA	TTAAAGGTGA	AAAATGAGTT
1910	1920	1930	1940	1950
TTCTCGTAAG	CGAGGAAAGT	CATTTTCCAT	GGAACGTAT	TTTTTTTTTA
1960	1970	1980	1990	2000
CTTTAATAA	CGTCATAGTA	TTGCTATAC	TCAAGAATAA	GACACTATTA
2010	2020	2030	2040	2050
TTGATGTTA	GTGCTCGAAA	AGAAATTGAT	AGTAATTG	CTAATATAAC
2060	2070	2080	2090	2100
TATCAATTTC	TTATATGTAT	ATTTTCAAC	CAAAATAACA	AAGCGTAATC
2110	2120	2130	2140	2150
CAATAAGTGG	GCCTCTAGAA	TAAAGAGTAA	GTTCTATTAA	TTCTTAACCT
2160	2170	2180	2190	2200
TATTTAATT	TATGGAAACC	TCGACAAAAC	GACAATGCTC	AACTTATATT

CGAATTC

FIGURE 8C

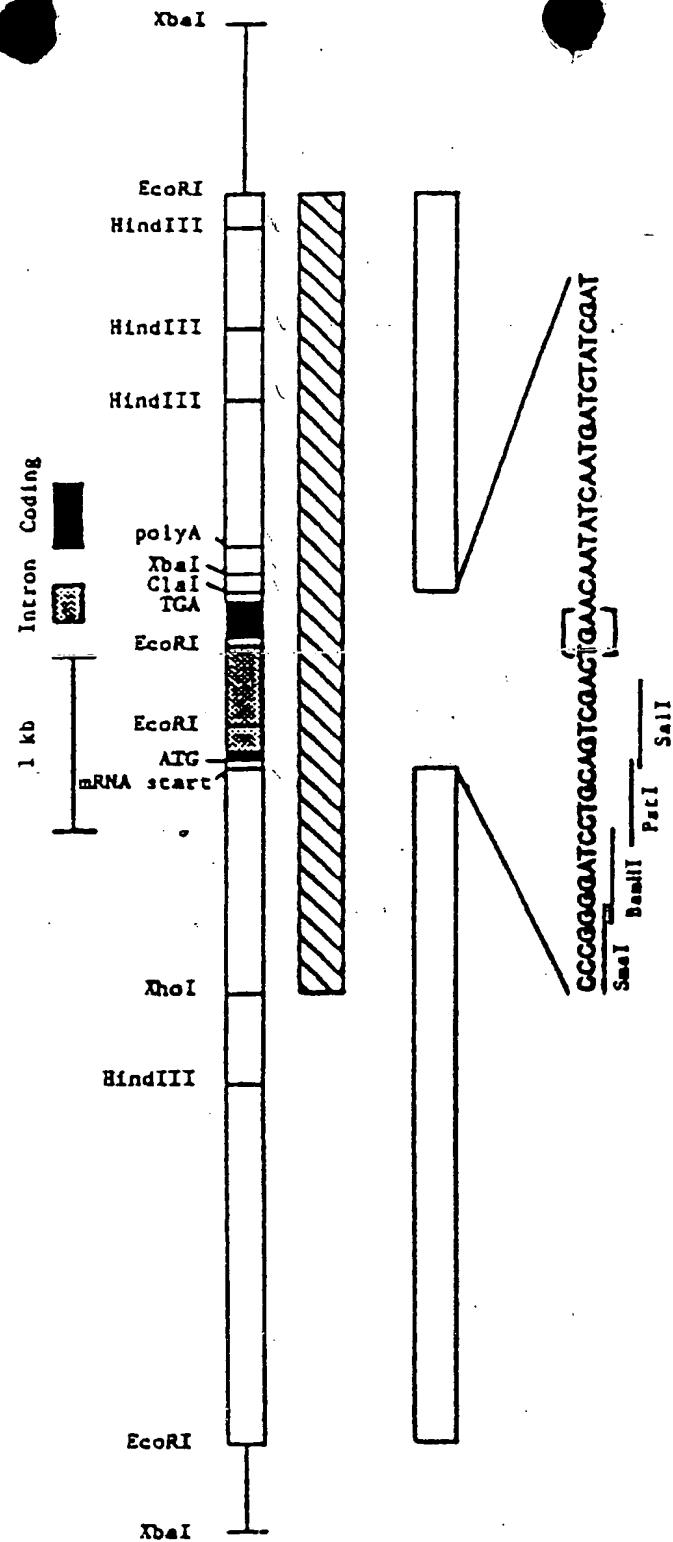


FIGURE 9

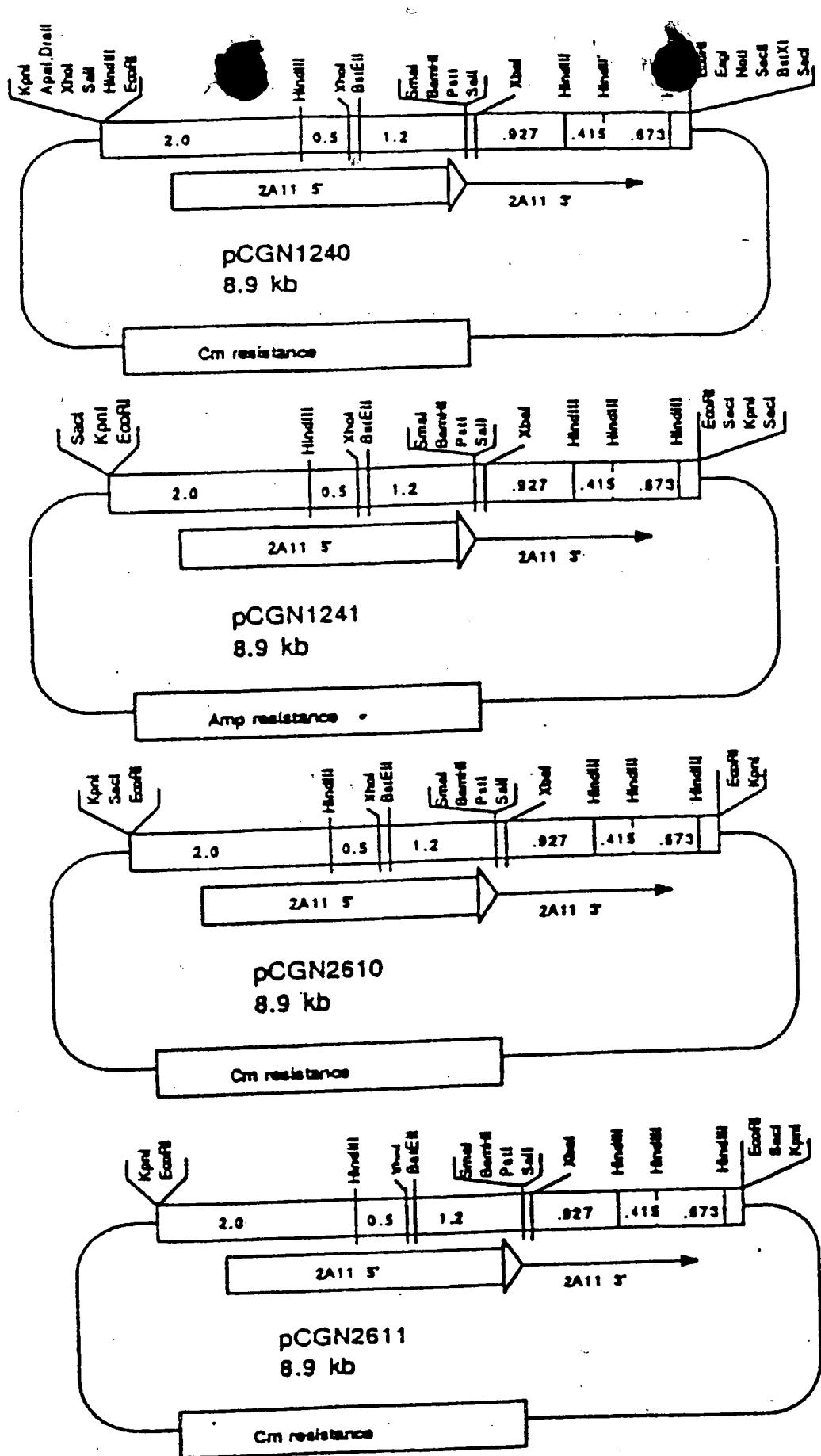


FIGURE 10